AMENDMENTS TO THE CLAIMS

Please cancel claims 17 and 18 without prejudice or disclaimer to the subject matter therein. These claims are cancelled solely for the purpose of advancing the prosecution of the present application. Applicants reserve the right to pursue the subject matter of these claims in a continuation application.

1-15. (Cancelled)

16. (Previously Presented) A method of constructing a set of promoter sequences which is suitable for optimizing the expression of a gene in a selected microorganism, said set of promoter sequences covering a range of promoter activities for said gene, the method comprising:

(i) identifying in said microorganism a promoter sequence comprising at least two consensus sequences, which consensus sequences correspond to conserved sequences identified in said microorganism, at least one of the consensus sequences being flanked by a non-conserved nucleotide spacer sequence or both of said consensus sequences being separated by the non-conserved nucleotide spacer sequence, the at least two consensus sequences, when the selected microorganism is

(a) a prokaryotic microorganism, wherein at least one of said at least two consensus sequences is TATAAT and at least one of said at least two consensus sequences is selected from the group consisting of TTGACA and an activator binding site upstream of the TATAAT sequence, or

(b) an eukayotic microorganism, wherein at least one of said at least two consensus sequences a TATA-box and at least one of said at least two consensus sequences is a UAS upstream of said TATA-box,

(ii) constructing a set of single stranded DNA sequences each of which comprises at least half of each of the consensus sequences, and a non-conserved nucleotide spacer sequence, at least part of which is varied by a random incorporation of nucleotides selected from the group consisting of the nucleobases A, T, C and G, whilst keeping the at least half of the consensus sequences constant, and

(iii) converting the single stranded DNA sequences into double stranded DNA sequences to obtain the set of promoter sequences covering a range of promoter activities for said gene.

17. (Cancelled)

18. (Cancelled)

19. (Cancelled)

20. (Cancelled)

21. (Cancelled)

22. (Previously Presented) An isolated promoter sequence selected from the group consisting of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID

NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:58.

23. (Cancelled)

24. (Cancelled)

25. (Cancelled)

26. (Cancelled)

27. (Cancelled)